GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 06:23:06 ; Search time 23795.2 Seconds
(without alignments)
972.809 Million cell updates/sec

Title: US-09-227-881-1
Perfect score: 5300
Sequence: 1 atctttgttcagtttacctc.....caggcacctctcagcacagc 5300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sy:*
14: gb_un:*
15: em_fun:*
16: em_hum1:*
17: em_hum2:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: gb_ba3:*
31: gb_in1:*
32: gb_in2:*
33: gb_in3:*
34: gb_pl3:*
35: gb_pr4:*
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37: em_ba2:*
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87: gb_htg20:*
88: gb_htg21:*
89: gb_htg22:*
90: gb_htg23:*
91: gb_sts1:*
92: gb_sts2:*
93: gb_vi1:*
94: gb_vi2:*

TIG

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	5286	99.7	79376	65	HS454G6	Z98750 Human DNA s
	2	5275.4	99.5	5300	11	AF007562	AF007562 Homo sapi
	3	5235	98.8	170425	77	AC024490	AC024490 Homo sapi
	4	1858	35.1	2800	66	HSMYOC1	AF049791 Homo sapi
	5	423.4	8.0	1086	66	HSGLC1A1	Z97171 Homo sapien
	6	423.4	8.0	1228	9	AB006686S1	AB006686 Homo sapi
c	7	189.8	3.6	161577	10	AC007688	AC007688 Homo sapi
c	8	189.8	3.6	193123	77	AC023790	AC023790 Homo sapi
	9	189	3.6	199722	71	AC012404	AC012404 Homo sapi
c	10	187.8	3.5	97037	9	AC004973	AC004973 Homo sapi
c	11	187.8	3.5	135038	67	HUMYWXD703	L78810 Homo sapien
c	12	185.8	3.5	76727	65	HS821D11	AL021453 Human DNA

c	13	185.8	3.5	152044	79	AC026395	AC026395 Homo sapi
c	14	185.8	3.5	157057	78	AC025947	AC025947 Homo sapi
	15	185.8	3.5	161499	72	AC015488	AC015488 Homo sapi
	16	185.8	3.5	184656	86	AL161726	AL161726 Homo sapi
	17	185.8	3.5	200681	69	AC008755	AC008755 Homo sapi
	18	185.6	3.5	201372	86	AL157941	AL157941 Homo sapi
	19	184.8	3.5	146190	89	AP001813	AP001813 Homo sapi
c	20	184.8	3.5	163494	89	AP002391	AP002391 Homo sapi
c	21	184.8	3.5	183241	89	AP001354	AP001354 Homo sapi
c	22	184.6	3.5	176029	11	AC011362	AC011362 Homo sapi
	23	184.2	3.5	130020	67	HUAC004525	AC004525 Homo sapi
	24	184	3.5	157304	78	AC024720	AC024720 Homo sapi
c	25	184	3.5	187709	73	AC016168	AC016168 Homo sapi
	26	184	3.5	233734	70	AC011407	AC011407 Homo sapi
	27	183.6	3.5	62070	88	AL358852	AL358852 Homo sapi
	28	183.6	3.5	129370	89	AP000609	AP000609 Homo sapi
c	29	183.6	3.5	169333	89	AP002789	AP002789 Homo sapi
c	30	183.6	3.5	193171	74	AC018723	AC018723 Homo sapi
	31	183.4	3.5	41407	11	AC053467	AC053467 Homo sapi
	32	183.4	3.5	149138	79	AC026936	AC026936 Homo sapi
	33	183.4	3.5	156331	90	HSJ193M11	AL121715 Homo sapi
c	34	183.4	3.5	174974	87	AL356055	AL356055 Homo sapi
c	35	183.4	3.5	195364	65	HS431A14	Z85996 Human DNA s
	36	183.4	3.5	198583	74	AC019114	AC019114 Homo sapi
	37	183.2	3.5	41936	35	CH19R30879	AD000684 Homo sapi
c	38	183.2	3.5	70128	10	AC007536	AC007536 Homo sapi
c	39	183.2	3.5	119483	9	AC005588	AC005588 Homo sapi
	40	183.2	3.5	145528	9	AC003665	AC003665 Homo sapi
	41	183.2	3.5	167943	65	HS267M20	AL031053 Human DNA
	42	183.2	3.5	170245	65	HS109F14	AL022721 Human DNA
c	43	183	3.5	42686	9	AC000093	AC000093 Homo sapi
	44	183	3.5	91767	10	AC007748	AC007748 Homo sapi
	45	183	3.5	112748	10	AC007242	AC007242 Homo sapi

ALIGNMENTS

RESULT 1
HS454G6/c
LOCUS HS454G6 79376 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains trabecular meshwork inducible glucocorticoid response protein, TIGR, myocilin, ESTs and STS.
ACCESSION Z98750
VERSION Z98750.1 GI:2887277
KEYWORDS 1q24; myocilin; TIGR.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 79376)
AUTHORS Deadman,R.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Feb 14, 1998 this sequence version replaced gi:2465060.
IMPORTANT: This sequence is not the entire insert of clone 454G6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The true left end of clone 454G6 is at 1 in this sequence. The true left end of clone 560B9 is at 79273.
454G6 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.

FEATURES Location/Qualifiers
source 1. .79376
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q24"
/clone="RP3-454G6"
/clone_lib="RPCI-3"
repeat_region 435. .472
/note="19 copies of 2 mer 82 % conserved"
prim_transcript 1914. .>3968
/note="match: multiple ESTs
match: R56676 AA043968 W63639 F12081 AA046699
match: F02925 AA131540 W00634 R36066 AA313383
match: AA163561 F02925 AA131540 W00634 R36066
match: AA313383 AA163561 N89173 AA174814 AA057059
match: AA329084 W47082 AA043955 AA341783 AA353681
match: AA046487 AA369741 H08313 AA186895 H32730
match: H08333 H08236 N42052 D61944 R27102 N32353
match: N30491 AA307150 AA192"
repeat_region 3703. .3746
/note="22 copies of 2 mer 89 % conserved"
repeat_region 4051. .4183
/note="AluSq repeat: matches 1. .133 of consensus incomplete repeat"
repeat_region 4200. .4502
/note="AluSq repeat: matches 2. .301 of consensus"
repeat_region 4659. .4851
/note="AluSx repeat: matches 2. .194 of consensus incomplete repeat"
repeat_region 5216. .5345
/note="AluJo repeat: matches 132. .1 of consensus incomplete repeat"
repeat_region 7759. .7907
/note="MIR repeat: matches 174. .1 of consensus"
repeat_region 7933. .9328
/note="TIGGER1 repeat: matches 1. .1472 of consensus"
repeat_region 9332. .9626
/note="AluSg repeat: matches 1. .289 of consensus"
repeat_region 9639. .10335
/note="TIGGER1 repeat: matches 1469. .2174 of consensus"
repeat_region 10343. .10642
/note="AluSp repeat: matches 1. .300 of consensus"
repeat_region 10643. .10856
/note="TIGGER1 repeat: matches 2175. .2417 of consensus"
misc_feature <10903. .>16855
/note="endogenous retroviral sequence"
repeat_region 10949. .11384
/note="LTR2 repeat: matches 31. .449 of consensus"
repeat_region 15835. .15870
/note="18 copies of 2 mer 83 % conserved"
repeat_region 16856. .17286
/note="LTR2 repeat: matches 31. .449 of consensus"
repeat_region 17287. .17574
/note="AluSg repeat: matches 15. .300 of consensus"
repeat_region 18294. .18650
/note="THE1B repeat: matches 358. .1 of consensus"
repeat_region 18877. .19180
/note="AluY repeat: matches 301. .2 of consensus"
repeat_region 19767. .20013
/note="MLT2_internal repeat: matches 5002. .4750 of consensus"

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repeat_region   20051. .20118
                /note="MLT1F repeat: matches 539. .471 of consensus"
repeat_region   20130. .20261
                /note="AluJb repeat: matches 131. .1 of consensus
                incomplete repeat"
repeat_region   20264. .20722
                /note="MLT1F repeat: matches 482. .1 of consensus"
repeat_region   20858. .21223
                /note="MSTD repeat: matches 394. .1 of consensus"
repeat_region   21216. .21302
                /note="MLT2_internal repeat: matches 4520. .4433 of
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repeat_region   21403. .21703
                /note="MLT2_internal repeat: matches 3887. .3580 of
                consensus"
repeat_region   21978. .22357
                /note="MLT2_internal repeat: matches 3218. .2839 of
                consensus"
repeat_region   22363. .22524
                /note="MLT2_internal repeat: matches 2495. .2317 of
                consensus"
repeat_region   22531. .22839
                /note="AluSx repeat: matches 302. .1 of consensus"
repeat_region   23007. .23309
                /note="AluSp repeat: matches 3. .301 of consensus"
misc_feature    23286. .>23680
                /note="STS G07544"
misc_feature    complement(23652. .24072)
                /note="STS G07436"
repeat_region   24008. .24290
                /note="AluJo repeat: matches 298. .6 of consensus"
repeat_region   25895. .26364
                /note="LTR2 repeat: matches 2. .449 of consensus"
repeat_region   26397. .26697
                /note="AluSq repeat: matches 1. .302 of consensus"
repeat_region   26719. .27021
                /note="AluSx repeat: matches 1. .302 of consensus"
repeat_region   29037. .29334
                /note="AluSx repeat: matches 300. .3 of consensus"
repeat_region   30028. .30310
                /note="AluSx repeat: matches 1. .301 of consensus"
repeat_region   30402. .30539
                /note="MLT2B repeat: matches 264. .404 of consensus"
repeat_region   30402. .30615
                /note="MLT2A repeat: matches 264. .453 of consensus"
prim_transcript <30801. .>31136
                /note="match: 5' EST AA256902 clone 682136"
repeat_region   30980. .31222
                /note="MER4B repeat: matches 199. .431 of consensus"
repeat_region   31232. .31528
                /note="AluSc repeat: matches 299. .1 of consensus"
repeat_region   31530. .31654
                /note="MER4B repeat: matches 417. .540 of consensus"
repeat_region   31836. .32135
                /note="AluY repeat: matches 300. .1 of consensus"
repeat_region   32200. .32301
                /note="AluJo repeat: matches 186. .287 of consensus
                incomplete repeat"
repeat_region   32365. .32493
                /note="MIR repeat: matches 206. .67 of consensus"
repeat_region   33283. .33399
                /note="MIR repeat: matches 77. .196 of consensus"
repeat_region   33408. .33667
                /note="AluY repeat: matches 1. .291 of consensus"
repeat_region   33956. .34043
                /note="MIR repeat: matches 80. .167 of consensus"
repeat_region   34725. .34904
                /note="AluJo repeat: matches 299. .127 of consensus
                incomplete repeat"
repeat_region   34907. .35207
                /note="AluY repeat: matches 300. .1 of consensus"
repeat_region   35212. .35344
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repeat_region   36545. .36842
                /note="AluJo repeat: matches 299. .1 of consensus"
repeat_region   38190. .38379
                /note="MER3 repeat: matches 209. .13 of consensus"
repeat_region   38382. .38682
                /note="AluSx repeat: matches 1. .302 of consensus"
repeat_region   38836. .38968
                /note="MIR2 repeat: matches 145. .2 of consensus"
repeat_region   38983. .39279
                /note="AluJb repeat: matches 3. .296 of consensus"
repeat_region   39418. .39773
                /note="THE1A repeat: matches 354. .2 of consensus"
repeat_region   39775. .40120
                /note="THE1B-INTERNAL repeat: matches 1580. .1234 of
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repeat_region   40757. .41023
                /note="AluJo repeat: matches 37. .301 of consensus
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repeat_region   41307. .41589
                /note="AluSq repeat: matches 21. .303 of consensus
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Query Match             99.7%;  Score 5286;  DB 65;  Length 79376;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 5298;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy      1 atctttgttcagtttacctcagggctattatgaaatgaaatgagataaccaatgtgaaag 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68406 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 68347

Qy     61 tcctataaactgtatagcctccattcggatgtatgtctttggcaggatgataaagaatca 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68346 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 68287

Qy    121 ggaagaaggagtatccacgttagccaagtgtccaggctgtgtctgctcttattttagtga 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68286 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 68227

Qy    181 cagatgttgctcctgacagaagctattcttcaggaaacatcacatccaatatggtaaatc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68226 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 68167

Qy    241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68166 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 68107

Qy    301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360
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Qy    361 atgaggaccaaaatcaatgaataaggaaaacagctcagaaaaaagatgtttccaaattgg 420
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Qy    421 taattaagtatttgttccttgggaagagacctccatgtgagcttgatgggaaaatgggaa 480
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Db  67986 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 67927

Qy    481 aaacgtcaaaagcatgatctgatcagatcccaaagtggattattatttttaaaaaccagat 540
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Db  67926 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTTAAAAACCAGAT 67867

Qy    541 ggcatcactctggggaggcaagttcaggaaggtcatgttagcaaaggacataacaataac 600
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Db  67866 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 67807

Qy    601 agcaaaatcaaaattccgcaaatgcaggaggaaaatggggactgggaaagctttcataac 660
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Db  67806 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 67747

Qy    661 agtgattaggcagttgaccatgttcgcaacacctccccgtctataccagggaacacaaaa 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67746 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 67687
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Qy    721 attgactgggctaagcctggactttcaagggaaatatgaaaaactgagagcaaaacaaaa 780
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Db  67686 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 67627

Qy    781 gacatggttaaaaggcaaccagaacattgtgagccttcaaagcagcagtgcccctcagca 840
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Db  67626 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 67567

Qy    841 gggaccctgaggcatttgcctttaggaaggccagttttcttaaggaatcttaagaaactc 900
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Db  67566 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 67507

Qy    901 ttgaaagatcatgaattttaaccattttaagtataaaacaaatatgcgatgcataatcag 960
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Db  67506 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 67447

Qy    961 tttagacatgggtcccaattttataaagtcaggcatacaaggataacgtgtcccagctcc 1020
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Db  67446 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 67387

Qy   1021 ggataggtcagaaatcattagaaatcactgtgtccccatcctaacttttcagaatgatc 1080
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Qy   1081 tgtcatagccctcacacacaggcccgatgtgtctgacctacaaccacatctacaacccaa 1140
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Qy   1141 gtgcctcaaccattgttaacgtgtcatctcagtaggtcccattacaaatgccacctcccc 1200
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Db  67266 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 67207

Qy   1201 tgtgcagcccatcccgctccacaggaagtctccccactctagacttctgcatcacgatgt 1260
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Db  67206 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 67147

Qy   1261 tacagccagaagctccgtgagggtgagggtctgtgtcttacacctacctgtatgctctac 1320
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Db  67146 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 67087

Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
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Qy   1381 cgcgtagctgggactacaggcgcacgcccggctaatttttgtattgttagtagagatggg 1440
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Db  67026 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 66967

Qy   1441 gtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatccacccacctc 1500
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Qy   1501 agcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaagggtcagtgt 1560
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Db  66906 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 66847

Qy   1561 ttaataaggaataacttgaatggtttactaaaccaacagggaaacagacaaaagctgtga 1620
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Qy   1621 taatttcagggattcttgggatggggaatggtgccatgagctgcctgcctagtcccagac 1680
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Qy   1921 tgggtgtcctgagcaacctgccagcccgtgccactggttgttttgttatcactctctagg 1980
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RESULT  2
AF007562
LOCUS       AF007562     5300 bp    DNA             PRI       18-MAR-1998
DEFINITION  Homo sapiens trabecular meshwork inducible glucocorticoid response
            protein (TIGR) gene, promoter region and partial mRNA sequence.
ACCESSION   AF007562
VERSION     AF007562.1  GI:2970123
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5300)
  AUTHORS   Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and
            Polansky,J.R.
  TITLE     Gene structure and properties of TIGR, an olfactomedin-related
            glycoprotein cloned from glucocorticoid-induced trabecular meshwork
            cells
  JOURNAL   J. Biol. Chem. 273 (11), 6341-6350 (1998)
  MEDLINE   98165818
REFERENCE   2  (bases 1 to 5300)
  AUTHORS   Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUN-1997) Ophthalmology, University of California San
            Francisco, 10 Kirkham Street, San Francisco, CA 94143-0730, USA
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BASE COUNT     1483 a   1152 c   1236 g   1429 t
ORIGIN


  Query Match             99.5%;  Score 5275.4;  DB 11;  Length 5300;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5298;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

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Db    181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy    241 catcaaacaggagctaagaaacaggaatgagatgggcacttgcccaaggaaaaatgccag 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy    301 gagagcaaataatgatgaaaaataaacttttccctttgtttttaatttcaggaaaaaatg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy    361 atgaggaccaaaatcaatgaataaggaaaacagctcagaaaaaagatgtttccaaattgg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy    421 taattaagtatttgttccttgggaagagacctccatgtgagcttgatgggaaaatgggaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy    481 aaacgtcaaaagcatgatctgatcagatcccaaagtggattattatttttaaaaaccagat 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTTAAAAACCAGAT 540

Qy    541 ggcatcactctggggaggcaagttcaggaaggtcatgttagcaaaggacataacaataac 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy    601 agcaaaatcaaaattccgcaaatgcaggaggaaaatggggactgggaaagctttcataac 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy    661 agtgattaggcagttgaccatgttcgcaacacctccccgtctataccagggaacacaaaa 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy    721 attgactgggctaagcctggactttcaagggaaatatgaaaaactgagagcaaaacaaaa 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy    781 gacatggttaaaaggcaaccagaacattgtgagccttcaaagcagcagtgcccctcagca 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy    841 gggaccctgaggcatttgccttaggaaggccagttttcttaaggaatcttaagaaactc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy    901 ttgaaagatcatgaatttaaccattttaagtataaaacaaatatgcgatgcataatcag 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy    961 tttagacatgggtcccaattttataaagtcaggcatacaaggataacgtgtcccagctcc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy   1021 ggataggtcagaaatcattagaaatcactgtgtccccatcctaacttttttcagaatgatc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy   1081 tgtcatagccctcacacacaggcccgatgtgtctgacctacaaccacatctacaacccaa 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy   1141 gtgcctcaaccattgttaacgtgtcatctcagtaggtcccattacaaatgccacctcccc 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy   1201 tgtgcagcccatcccgctccacaggaagtctccccactctagacttctgcatcacgatgt 1260
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Db   1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy   1261 tacagccagaagctccgtgagggtgagggtctgtgtcttacacctacctgtatgctctac 1320
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Db   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy   1381 cgcgtagctgggactacaggcgcacgcccggctaatttttgtattgttagtagagatggg 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy   1441 gtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatccacccacctc 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy   1501 agcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaagggtcagtgt 1560
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Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy   1561 ttaataaggaataacttgaatggtttactaaaccaacagggaaacagacaaaagctgtga 1620
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Db   1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy   1621 taatttcagggattcttgggatggggaatggtgccatgagctgcctgcctagtcccagac 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy   1681 cactggtcctcatcactttcttccctcatcctcattttcaggctaagttaccatttttatt 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy   1741 caccatgcttttgtggtaagcctccacatcgttactgaaataagagtatacataaactag 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy   1801 ttccatttggggccatctgtgtgtgtgtataggggaggagggcataccccagagactcct 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy   1861 tgaagcccccggcagaggtttcctctccagctgggggagccctgcaagcacccggggtcc 1920
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Db   1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy   1921 tgggtgtcctgagcaacctgccagcccgtgccactggttgttttgttatcactctctagg 1980
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Db   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy   1981 gacctgttgctttctatttctgtgtgactcgttcattcatccaggcattcattgacaatt 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy   2041 tattgagtacttatatctgccagacaccagagacaaaatggtgagcaaagcagtcactgc 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy   2101 cctaccttcgtggaggtgacagtttctcatggaagacgtgcagaagaaaattaatagcca 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy   2161 gccaacttaaacccagtgctgaaagaaaggaaataaacaccatcttgaagaattgtgcgc 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy   2221 agcatcccttaacaaggccacctccctagcgcccccctgctgcctccatcgtgcccggagg 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy   2281 cccccaagcccgagtcttccaagcctcctcctccatcagtcacagcgctgcagctggcct 2340
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Db   2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy   2341 gcctcgcttcccgtgaatcgtcctggtgcatctgagctggagactccttggctccaggct 2400
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Db   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy   2401 ccagaaaggaaatggagagggaaactagtctaacggagaatctggaggggacagtgtttc 2460
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Qy   2461 ctcagagggaaaggggcctccacgtccaggagaattccaggaggtggggactgcagggag 2520
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Qy   2521 tggggacgctggggctgagcgggtgctgaaaggcaggaaggtgaaaagggcaaggctgaa 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy   2581 gctgcccagatgttcagtgttgttcacggggctgggagttttccgttgcttcctgtgagc 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy   2641 ctttttatcttttctctgcttggaggagaagaagtctatttcatgaagggatgcagtttc 2700
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Db   2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy   2701 ataaagtcagctgttaaaattccagggtgtgcatgggttttccttcacgaaggcctttat 2760
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Qy   2821 tggagtcttttctttcatgtcttctgggcaactactcagccctgtggtggacttggctta 2880
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Qy   2881 tgcaagacggtcgaaaaccttggaatcaggagactcggttttctttctggttctgccatt 2940
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Qy   2941 ggttggctgtgcgaccgtgggcaagtgtctctccttccctgggccatagtcttctctgct 3000
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Db   2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy   3001 ataaagaccttgcagctctcgtgttctgtgaacacttccctgtgattctctgtgagggg 3060
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Qy   3061 ggatgttgagaggggaaggaggcagagctggagcagctgagccacaggggaggtggaggg 3120
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Qy   3121 ggacaggaaggcaggcagaagctgggtgctccatcagtcctcactgatcacgtcagactc 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy   3181 caggaccgagagccacaatgcttcaggaaagctcaatgaacccaacagccacattttcct 3240
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Qy   3241 tccctaagcatagacaatggcatttgccaataaccaaaaagaatgcagagactaactggt 3300
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Qy   3301 ggtagcttttgcctggcattcaaaaactgggccagagcaagtggaaaatgccagagattg 3360
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Qy   3361 ttaaacttttcaccctgaccagcaccccacgcagctcagcagtgactgctgacagcacgg 3420
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Qy   3421 agtgacctgcagcgcaggggaggagaagaaaaagagagggatagtgtatgagcaagaaag 3480
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Qy   3601 cctgatttctaatactatatttttcctttacaagctgagtaattctgagcaagtcacaag 3660
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Qy   3841 catttcagcgatgtttactatctgattcagaaaatgagactagtaccctttggtcagctg 3900
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Qy   3901 taaacaaacacccatttgtaaatgtctcaagttcaggcttaactgcagaaccaatcaaat 3960
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Qy   3961 aagaatagaatctttagagcaaactgtgtttctccac-tctggaggtgagtctgccaggg 4019
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Qy   4020 cagtttggaaatatttacttcacaagtattgacactgttgttggtattaacaacataaag 4079
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Qy   4080 ttgctcaaaggcaatcattatttcaagtggcttaaagttacttctgacagttttggtata 4139
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Qy   4140 tttattggctattgccatttgctttttgtttttttctctttgggtttattaatgtaaagca 4199
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Db   4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy   4200 gggattattaacctacagtccagaaagcctgtgaatttgaatgaggaaaaaattacattt 4259
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Qy   4260 ttgtttttaccaccttctaactaaatttaacatttttattccattgcgaatagagccataa 4319
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Qy   4320 actcaaagtggtaataacagtacctgtgattttgtcattaccaatagaaatcacagacat 4379
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Qy   4380 tttatactatattacagttgttgcagatacgttgtaagtgaaatatttatactcaaaact 4439
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Db   4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy   4440 actttgaaattagacctcctgctggatcttgtttttaacatattaataaaacatgtttaa 4499
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Db   4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
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Qy   4500 aattttgatattttgataatcatatttcattatcatttgtttccttttgtaatctatattt 4559
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Db   4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy   4560 tatatatttgaaaacatctttctgagaagagttccccagatttcaccaatgaggttcttg 4619
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Qy   4620 gcatgcacacacacagagtaagaactgatttagaggctaacattgacattggtgcctgag 4679
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Qy   4680 atgcaagactgaaattagaaagttctcccaaagatacacagttgttttaaagctaggggt 4739
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DEFINITION  Homo sapiens chromosome 1 clone RP11-138F3 map 1, WORKING DRAFT
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ACCESSION   AC024490
VERSION     AC024490.3  GI:8076950
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
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  TITLE     Homo sapiens chromosome 1, clone RP11-138F3
  JOURNAL   Unpublished
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REFERENCE   2  (bases 1 to 170425)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
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            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 25, 2000 this sequence version replaced gi:7249345.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L7153
                Center clone name: 138_F_3
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 151483 bases at least Q40
                Consensus quality: 160439 bases at least Q30
                Consensus quality: 164708 bases at least Q20
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                Insert size: 167725; sum-of-contigs
                Quality coverage: 4.1 in Q20 bases; agarose-fp
                Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 28 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
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ORIGIN
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Matches 5288; Conservative 0; Mismatches 10; Indels 7; Gaps 4;

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RESULT   4
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LOCUS       HSMYOC1      2800 bp    DNA             PRI       21-APR-1998
DEFINITION  Homo sapiens myocilin (GLC1A) gene, promoter and exon 1.
ACCESSION   AF049791
VERSION     AF049791.1  GI:3065670
KEYWORDS    .
SEGMENT     1 of 3
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2800)
  AUTHORS   Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
            Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
  TITLE     Characterization and comparison of the human and mouse GLC1A
            glaucoma genes
  JOURNAL   Genome Res. (1998) In press
REFERENCE   2  (bases 1 to 2800)
  AUTHORS   Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
            Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200
            Hawkins Drive, Iowa City, IA 52242, USA
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ORIGIN
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Db    900 TAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTATA 959

Qy   4391 ttacagttgttgcagatacgttgtaagtgaaatatttatactcaaaactactttgaaatt 4450
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Db    960 TTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAATT 1019

Qy   4451 agacctcctgctggatcttgtttttaacatattaataaaacatgtttaaaattttgatat 4510
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Db   1020 AGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATAT 1079

Qy   4511 tttgataatcatatttcattatcatttgtttcctttgtaatctatattttatatatttga 4570
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Db   1080 TTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTGA 1139

Qy   4571 aaacatctttctgagaagagttccccagatttcaccaatgaggttcttggcatgcacaca 4630
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Db   1140 AAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACACA 1199

Qy   4631 cacagagtaagaactgatttagaggctaacattgacattggtgcctgagatgcaagactg 4690
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Db   1200 CACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACTG 1259

Qy   4691 aaattagaaagttctcccaaagatacacagttgttttaaagctaggggtgaggggggaaa 4750
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Db   1260 AAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAAA 1319

Qy   4751 tctgccgcttctataggaatgctctccctggagcctggtagggtgctgtccttgtgttct 4810
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Qy   4811 ggctggctgttatttttctctgtccctgctacgtcttaaaggacttgtttggatctccag 4870
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Db   1380 GGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCAG 1439

Qy   4871 ttcctagcatagtgcctggcacagtgcaggttctcaatgagtttgcagagtgaatggaaa 4930
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Qy   4931 tataaactagaaatatatccttgttgaaatcagcacaccagtagtcctggtgtaagtgtg 4990
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Db   1500 TATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGTG 1559

Qy   4991 tgtacgtgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagatataggaactat 5050
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Db   1560 TGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTAT 1619

Qy   5051 tattggggtatgggtgcataaattgggatgttctttttaaaaagaaactccaaacagact 5110
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Qy   5111 tctggaaggttattttctaagaatcttgctggcagcgtgaaggcaaccccccctgtgcaca 5170
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Db   1680 TCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCACA 1739

Qy   5171 gccccacccagcctcacgtggccacctctgtcttcccccatgaagggctggctccccagt 5230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 GCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAGT 1799

Qy   5231 atatataaacctctctggagctcgggcatgagccagcaaggccacccatccaggcacctc 5290
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 ATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGGCCACCCATCCAGGCACCTC 1859

Qy   5291 tcagcacagc 5300
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Db   1860 TCAGCACAGC 1869
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HSGLC1A1
LOCUS       HSGLC1A1     1086 bp    DNA             PRI       30-JAN-1998
DEFINITION  Homo sapiens GLC1A (trabecular meshwork induced glucocortcoid
            response) gene, exon I, joined CDS.
ACCESSION   Z97171
VERSION     Z97171.1  GI:2425156
KEYWORDS    GLC1A.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1086)
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  AUTHORS   Stone,E.M., Fingert,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R.,
            Sunden,S.L., NIshimura,D., Clark,A.F., Nystuen,A., Nichols,B.E.,
            Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C.
  TITLE     Identification of a gene that causes primary open angle glaucoma
  JOURNAL   Science 275 (5300), 668-670 (1997)
  MEDLINE   97158493
REFERENCE   2  (bases 1 to 1086)
  AUTHORS   Adam,M.F., Belmouden,A., Binisti,P., Brezin,A.P., Valtot,F.,
            Bechetoille,A., Dascotte,J.C., Copin,B., Gomez,L., Chaventre,A.,
            Bach,J.F. and Garchon,H.J.
  TITLE     Recurrent mutations in a single exon encoding the evolutionarily
            conserved olfactomedin-homology domain of TIGR in familial
            open-angle glaucoma
  JOURNAL   Hum. Mol. Genet. 6 (12), 2091-2097 (1997)
  MEDLINE   97472461
REFERENCE   3  (bases 1 to 1086)
  AUTHORS   Garchon,H.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-1997) Garchon H.-J., Hopital Necker, INSERM U25,
            161 rue de Sevres 75743 Paris cedex 15 FRANCE
FEATURES             Location/Qualifiers
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                     /tissue_type="white blood cells"
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                     /label=ex1
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                     /note="first coding exon"
                     /label=start
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                     /db_xref="GI:2425157"
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ORIGIN


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  Best Local Similarity   99.8%;  Pred. No. 9.6e-81;
  Matches  424;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   4876 agcatagtgcctggcacagtgcaggttctcaatgagtttgcagagtgaatggaaatataa 4935
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Db      1 AGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAAATATAA 60

Qy   4936 actagaaatatatccttgttgaaatcagcacaccagtagtcctggtgtaagtgtgtgtac 4995
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Db     61 ACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGTGTGTAC 120

Qy   4996 gtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagatataggaactattattg 5055
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Db    121 GTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTATTATTG 180

Qy   5056 gggtatgggtgcataaattgggatgttctttttaaaaagaaactccaaacagacttctgg 5115
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Db    181 GGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGACTTCTGG 240

Qy   5116 aaggttattttctaagaatcttgctggcagcgtgaaggcaacccccctgtgcacagcccc 5175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCACAGCCCC 300

Qy   5176 acccagcctcacgtggccacctctgtcttcccccatgaagggctggctccccagtatata 5235
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Db    301 ACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAGTATATA 360

Qy   5236 taaacctctctggagctcgggcatgagccagcaaggccacccatccaggcacctctcagc 5295
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Db    361 TAAACCTCTCTGGAGCTCGGGCATGAGCCACCAAGGCCACCCATCCAGGCACCTCTCAGC 420

Qy   5296 acagc 5300
           |||||
Db    421 ACAGC 425


RESULT   6
AB006686S1
LOCUS       AB006686S1   1228 bp    DNA             PRI       14-APR-2000
DEFINITION  Homo sapiens gene for myocilin, exon 1, complete sequence.
ACCESSION   AB006686
VERSION     AB006686.1  GI:2828342
KEYWORDS    myocilin.
SEGMENT     1 of 3
SOURCE      Homo sapiens pre-pro-B cell cell_line:FLEB14-14 DNA, clone_lib:BAC
            clone:KB780C12.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Escribano,J., Ortego,J. and Coca-Prados,M.
  TITLE     Isolation and characterization of cell-specific cDNA clones from a
            subtractive library of the ocular ciliary body of a single normal
            human donor: transcription and synthesis of plasma proteins
  JOURNAL   J. Biochem. 118 (5), 921-931 (1995)
  MEDLINE   96318503
REFERENCE   2  (sites)
  AUTHORS   Stone,E.M., Fingert,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R.,
            Sunden,S.L., NIshimura,D., Clark,A.F., Nystuen,A., Nichols,B.E.,
            Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C.
  TITLE     Identification of a gene that causes primary open angle glaucoma
  JOURNAL   Science 275 (5300), 668-670 (1997)
  MEDLINE   97158493
REFERENCE   3  (sites)
  AUTHORS   Kubota,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J.,
            Mashima,Y., Oguchi,Y. and Shimizu,N.
  TITLE     A novel myosin-like protein (myocilin) expressed in the connecting
            cilium of the photoreceptor: molecular cloning, tissue expression,
            and chromosomal mapping
  JOURNAL   Genomics 41 (3), 360-369 (1997)
  MEDLINE   97312692
REFERENCE   4  (sites)
  AUTHORS   Kubota,R., Kudoh,J., Mashima,Y., Asakawa,S., Minoshima,S.,
            Hejtmancik,J.F., Oguchi,Y. and Shimizu,N.
  TITLE     Genomic organization of the human myocilin gene (MYOC) responsible
            for primary open angle glaucoma (GLC1A)
  JOURNAL   Biochem. Biophys. Res. Commun. 242 (2), 396-400 (1998)
  MEDLINE   98113364
REFERENCE   5  (bases 1 to 1228)
  AUTHORS   Shimizu,N. and Kudoh,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-1997) to the DDBJ/EMBL/GenBank databases.
            Nobuyoshi Shimizu, Keio University School of Medicine, Department
            of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582,
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            Japan (E-mail:shimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370(ex.2720), Fax:81-3-3351-2370)
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                     /clone_lib="BAC"
                     /map="1q23-q24"
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                     /note="glucocorticoid responsive element consensus
                     sequence"
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     exon            431. .1077
                     /number=1
                     /product="myocilin"
BASE COUNT      312 a    325 c    350 g    241 t
ORIGIN

  Query Match             8.0%;  Score 423.4;  DB 9;  Length 1228;
  Best Local Similarity   99.3%;  Pred. No. 9.6e-81;
  Matches  436;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy   4862 gatctccagttcctagcatagtgcctggcacagtgcaggttctcaatgagtttgcagagt 4921
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Db      1 GATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGT 60

Qy   4922 gaatggaaatataaactagaaatatatccttgttgaaatcagcacaccagtagtcctggt 4981
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Db     61 GAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGT 120

Qy   4982 gtaagtgtgtgtacgtgtgtgtgtgtgtgtgtgtgtgtgtaaaaccaggtggagatat 5041
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Db    121 GTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATAT 178

Qy   5042 aggaactattattggggtatgggtgcataaattgggatgttctttttaaaaagaaactcc 5101
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Db    179 AGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCC 238

Qy   5102 aaacagacttctggaaggttattttctaagaatcttgctggcagcgtgaaggcaaccccc 5161
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Db    239 AAACAGACTTCCGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCC 298

Qy   5162 ctgtgcacagccccacccagcctcacgtggccacctctgtcttcccccatgaagggctgg 5221
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Db    299 CTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGG 358

Qy   5222 ctccccagtatatataaacctctctggagctcgggcatgagccagcaaggccacccatcc 5281
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Db    359 CTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGGCCACCCATCC 418

Qy   5282 aggcacctctcagcacagc 5300
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Db    419 AGGCACCTCTCAGCACAGC 437


RESULT   7
AC007688/c
LOCUS       AC007688   161577 bp    DNA             PRI       01-SEP-1999
DEFINITION  Homo sapiens 12p12-27.2-31.7 BAC RPCI11-392P7 (Roswell Park Cancer
            Institute Human BAC Library) complete sequence.
ACCESSION   AC007688
VERSION     AC007688.15  GI:5815499
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 161577)
  AUTHORS   Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
            Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,
            Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,
            Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W.,
            Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A.,
            Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
            Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,
            Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W.,
            Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 161577)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1999) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 161577)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 1, 1999 this sequence version replaced gi:5757565.
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent clones.
            Overlapping clones are noted at the beginning and end of the
            Features listing.

            ANNOTATION OF FEATURES:
               STSs are identified using ePCR (Genome Res. 7:541-550) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
               Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
               Genes and Region of sequence similarity are identified by BLAST
            (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of 2 clones and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and 3 reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as Low Coverage.

            QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
            standards - estimated error rate less than 1 per 10,000 bases.
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
            html.

            QUALSTAT-REPORT----------


            ---------- Summary Statistics ------------------------------
            Contig length:                                  161577
            Phrap values in estimate:                       160751
            Average error rate (BCM-Phrap estimate):        0.000163681
            Fraction of Phrap values less than 40 :         0.0376047
            Number of consensus changing edits:             30
            Number of N's in consensus :                    0


            ---------- Consensus changing edits ------------------------
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Position	Original+Context	Edited+Context
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47567	aaaaaaaaaa(n)ggaaaataat	aaaaaaaaaa(a)ggaaaataat
51135	aaagaaagaa(n)aaagaaggaa	aaagaaagaa(a)aaagaaggaa
75582	aaaaaaaaaa(n)aanggatgtt	aaaaaaaaaa(a)aaaggatgtt
75585	aaaaaaanaa(n)ggatgttcgc	aaaaaaaaaa(a)ggatgttcgc
75667	ctaaagcaga(n)taagatctta	ctaaagcaga(a)taagatctta
75752	ttttaaatag(g)gctttgcttt	ttttaaatag(t)gctttgcttt
84017	gggagggaag(n)aaggaaggag	gggagggaag(g)aaggaaggag
85227	ttttgttttt(n)tgttttttt	ttttgttttt(t)tgttttttt
99681	ggagttcaag(n)atgcagtgag	ggagttcaag(g)atgcagtgag
111307	aatctcttat(n)cccgaattca	aatctcttat(g)cccgaattca
111374	actagtatac(n)atcnttttt	actagtatac(t)atcctttttt
111378	gtatacnatc(n)ttttttttt	gtatactatc(c)ttttttttt
112621	aaaaaaaaaa(n)ccatcctaga	aaaaaaaaaa(a)ccatcctaga
135812	attcaccctc(c)ttttttttt	attcaccctc(t)ttttttttt
137207	ttgcaggcac(n)cgccaccacg	ttgcaggcac(a)cgccaccacg
137218	cgccaccacg(n)ctggctaagt	cgccaccacg(c)ctggctaagt
145113	gcaagtgaaa(n)natgtagaat	gcaagtgaaa(a)gatgtagaat
145114	caagtgaaan(n)atgtagaata	caagtgaaaa(g)atgtagaata
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145233	gcaccggtgn(n)tcacnccagt	gcaccggtgc(c)tcacgccagt
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145321	gcaacatggt(t)nnncccccatc	gcaacatggt(g)aaaccccatc
145322	caacatggtt(n)nnccccatct	caacatggtg(a)aaccccatct
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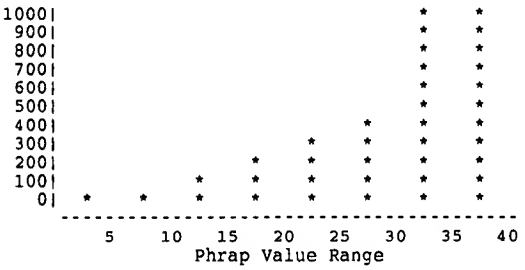
145324	acatggttnn(n)ccccatctct	acatggtgaa(a)ccccatctct
145363	gttcaccagg(n)gtggtggcgt	gttcaccagg(t)gtggtggcgt
145377	gtggcgtgta(t)ttgtagtcct	gtggcgtgta(g)ttgtagtcct
145397	tagctacttg(n)gagggaggat	tagctacttg(g)gagggaggat
145505	aaaaaaaaaa(n)gaaaaaaaaa	aaaaaaaaaa(a)gaaaaaaaaa

--------- Distribution of Quality < 40 Bases ----------



Version: 1.01 qxfo.

FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/chromosome="12p13.3"
	/clone="RPCI11-392P7"
repeat_region	complement(3. .65)
	/rpt_family="MER4B"
repeat_region	161. .471
	/rpt_family="AluSx"
repeat_region	complement(607. .702)
	/rpt_family="MIR"
repeat_region	703. .838
	/rpt_family="FLAM_C"
repeat_region	complement(839. .916)
	/rpt_family="MIR"
repeat_region	complement(1205. .1377)
	/rpt_family="MER104"
STS	1388. .1525
	/standard_name="WIAF-759-STS"
	/db_xref="dbSTS:65358"
repeat_region	1683. .1971
	/rpt_family="AluJo"
repeat_region	1974. .2261
	/rpt_family="AluJb"
repeat_region	2486. .2593
	/rpt_family="MIR"
misc_feature	2610. .3214
	/note="Region: Unigene cluster similar to AA056332 and AI074576."
STS	2712. .2823
	/standard_name="SHGC-44583"
	/db_xref="dbSTS:48451"
repeat_region	3185. .3491
	/rpt_family="AluSq"
gene	4509. .5919
	/gene="Human 5-hydroxytryptamine7 receptor isoform b mRNA, U68487."
repeat_region	complement(6397. .6537)
	/rpt_family="L2"
repeat_region	6967. .7158
	/rpt_family="(CCCCG)n"
repeat_region	7094. .7240
	/rpt_family="(CCG)n"
gene	join(7241. .7357,17979. .18117,20062. .20242,23659. .23933)
	/gene="Unigene cluster containing N42239, R09325, and AI380369."
repeat_region	complement(7770. .8250)
	/rpt_family="MER44B"
repeat_region	8831. .9073
	/rpt_family="MER102"
repeat_region	complement(9075. .9303)
	/rpt_family="L2"
repeat_region	9671. .10135
	/rpt_family="LTR33A"
repeat_region	10426. .10592
	/rpt_family="MIR"
repeat_region	10625. .10689
	/rpt_family="MIR"
repeat_region	11094. .11322
	/rpt_family="MIR"
repeat_region	complement(11985. .12403)
	/rpt_family="L2"

Query Match 3.6%; Score 189.8; DB 10; Length 161577;
Best Local Similarity 78.5%; Pred. No. 9.9e-31;
Matches 227; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Qy   1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
          || ||     ||| |  |  |  |  || |     |   | ||  ||||| |||||||
Db  29160 AGAGTCTCACTCTATTACCCAGGCTGAAGTGCAGTGGCGCAATCTCGGCTCATTGCAACC 29101

Qy   1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
          ||||||||||||||||||  |||||||| || ||| ||||| ||||||||||||||||
Db  29100 TCTGCCTCCCAGGTTCAAGTGATTCTCCTGCCTTAGCTTCCCGAGTAGCTGGGACTACAG 29041

Qy   1400 gcgcacgcccggctaatttttgtattgttagtagagatggggtttcaccatattagcccg 1459
          || ||||||| |||||||||||||||| |||||| ||||||||||  || |||| ||| |
Db  29040 GCACACGCCCAGCTAATTTTTGTATTTTTAGTACAGATGGGGTTTTGCCGTATTGGCCAG 28981

Qy   1460 gctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaagtgctggg 1519
          ||||||||  |||||||||||||||||||||||||| |||||||||||||||||||||||
Db  28980 GCTGGTCTCAAACTCCTGACCTCAGGTGATCCACCCGCCTCAGCCTCCTAAAGTGCTGGG 28921

Qy   1520 attacaggcatgagtcaccgcgcccggccaagggtcagtgtttaataag 1568
          ||||||||  |||| |||| |||||||||  |     || || ||  ||
Db  28920 ATTACAGGTGTGAGCCACCACGCCCGGCCTGGAAAGGGTTTTAAAGTAG 28872
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RESULT 8
AC023790/c
LOCUS AC023790 193123 bp DNA HTG 25-JUL-2000
DEFINITION Homo sapiens chromosome 12 clone RP11-377D9, WORKING DRAFT

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           SEQUENCE, 35 unordered pieces.
ACCESSION  AC023790
VERSION    AC023790.16  GI:9438256
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     human.
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 193123)
  AUTHORS  Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K.,
           Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
           Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
           David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
           Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
           Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
           Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
           Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
           Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
           Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J.,
           Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
           Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
           Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
           Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
           Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
           Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M.,
           Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
           Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
           Gibbs,R.
  TITLE    Direct Submission
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 193123)
  AUTHORS  Worley,K.C.
  TITLE    Direct Submission
  JOURNAL  Submitted (18-FEB-2000) Human Genome Sequencing Center, Department
           of Molecular and Human Genetics, Baylor College of Medicine, One
           Baylor Plaza, Houston, TX 77030, USA
COMMENT    On Jul 25, 2000 this sequence version replaced gi:9255941.
           -------------- Genome Center
              Center: Baylor College of Medicine
              Center code: BCM
              Web site: http://www.hgsc.bcm.tmc.edu/
              Contact: hgsc-help@bcm.tmc.edu
           -------------- Project Information
              Center project name: HABM
              Center clone name: RP11-377D9
           -------------- Summary Statistics
              Assembly program: Phrap; version 0.990329
              Consensus quality: 167304 bases at least Q40
              Consensus quality: 176244 bases at least Q30
              Consensus quality: 181341 bases at least Q20
              Estimated insert size: 180060; sum-of-contigs estimation
              Quality coverage: 0x in Q20 bases; agarose-fp estimation
              Quality coverage: 3.1x in Q20 bases; sum-of-contigs estimation
           --------------
           * NOTE: Estimated insert size may differ from sequence length
           *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 35 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           *        1    21094: contig of 21094 bp in length
           *    21095    21194: gap of unknown length
           *    21195    33930: contig of 12736 bp in length
           *    33931    34030: gap of unknown length
           *    34031    48318: contig of 14288 bp in length
           *    48319    48418: gap of unknown length
           *    48419    58799: contig of 10381 bp in length
           *    58800    58899: gap of unknown length
           *    58900    68723: contig of 9824 bp in length
           *    68724    68823: gap of unknown length
           *    68824    76073: contig of 7250 bp in length
           *    76074    76173: gap of unknown length
           *    76174    82868: contig of 6695 bp in length
           *    82869    82968: gap of unknown length
           *    82969    90046: contig of 7078 bp in length
           *    90047    90146: gap of unknown length
           *    90147    96141: contig of 5995 bp in length
           *    96142    96241: gap of unknown length
           *    96242   101873: contig of 5632 bp in length
           *   101874   101973: gap of unknown length
           *   101974   108002: contig of 6029 bp in length
           *   108003   108102: gap of unknown length
           *   108103   112903: contig of 4801 bp in length
           *   112904   113003: gap of unknown length
           *   113004   120209: contig of 7206 bp in length
           *   120210   120309: gap of unknown length
           *   120310   126353: contig of 6044 bp in length
           *   126354   126453: gap of unknown length
           *   126454   132888: contig of 6435 bp in length
           *   132889   132988: gap of unknown length
           *   132989   140137: contig of 7149 bp in length
           *   140138   140237: gap of unknown length
           *   140238   144631: contig of 4394 bp in length
           *   144632   144731: gap of unknown length
           *   144732   150312: contig of 5581 bp in length
           *   150313   150412: gap of unknown length
           *   150413   154114: contig of 3702 bp in length
           *   154115   154214: gap of unknown length
           *   154215   158458: contig of 4244 bp in length
           *   158459   158558: gap of unknown length
           *   158559   161385: contig of 2827 bp in length
           *   161386   161485: gap of unknown length
           *   161486   164320: contig of 2835 bp in length
           *   164321   164420: gap of unknown length
           *   164421   167714: contig of 3294 bp in length
           *   167715   167814: gap of unknown length
           *   167815   171014: contig of 3200 bp in length
           *   171015   171114: gap of unknown length
           *   171115   173843: contig of 2729 bp in length
           *   173844   173943: gap of unknown length
           *   173944   176631: contig of 2688 bp in length
           *   176632   176731: gap of unknown length
           *   176732   178648: contig of 1917 bp in length
           *   178649   178748: gap of unknown length
           *   178749   180232: contig of 1484 bp in length
           *   180233   180332: gap of unknown length
           *   180333   183104: contig of 2772 bp in length
           *   183105   183204: gap of unknown length
           *   183205   184720: contig of 1516 bp in length
           *   184721   184820: gap of unknown length
           *   184821   186137: contig of 1317 bp in length
           *   186138   186237: gap of unknown length
           *   186238   188213: contig of 1976 bp in length
           *   188214   188313: gap of unknown length
           *   188314   190073: contig of 1760 bp in length
           *   190074   190173: gap of unknown length
           *   190174   191855: contig of 1682 bp in length
           *   191856   191955: gap of unknown length
           *   191956   193123: contig of 1168 bp in length.
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                     /db_xref="taxon:9606"
                     /chromosome="12"
                     /clone="RP11-377D9"
BASE COUNT    54294 a  41007 c  41291 g  53110 t   3421 others
ORIGIN


  Query Match             3.6%;  Score 189.8;  DB 77;  Length 193123;
  Best Local Similarity   78.5%;  Pred. No. 1e-30;
  Matches  227;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;
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Qy   1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
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Db 134698 AGAGTCTCACTCTATTACCCAGGCTGAAGTGCAGTGGCGCAATCTCGGCTCATTGCAACC 134639

Qy   1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
          ||||||||||||||||||  |||||||||| || ||| ||||| ||||||||||||||||
Db 134638 TCTGCCTCCCAGGTTCAAGTGATTCTCCTGCCTTAGCTTCCCGAGTAGCTGGGACTACAG 134579

Qy   1400 gcgcacgcccggctaatttttgtattgttagtagagatggggtttcaccatattagcccg 1459
          || |||||| ||||||||||||||| |||||| |||||||||||  || |||| ||| |
Db 134578 GCACACGCCCAGCTAATTTTTGTATTTTTAGTACAGATGGGGTTTTGCCGTATTGGCCAG 134519

Qy   1460 gctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaagtgctggg 1519
          ||||||||  ||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 134518 GCTGGTCTCAAACTCCTGACCTCAGGTGATCCACCCGCCTCAGCCTCCTAAAGTGCTGGG 134459

Qy   1520 attacaggcatgagtcaccgcgcccggccaagggtcagtgtttaataag 1568
          ||||||||  |||| |||| |||||||||  |     || || ||  ||
Db 134458 ATTACAGGTGTGAGCCACCACGCCCGGCCTGGAAAGGGTTTTAAAGTAG 134410


RESULT   9
AC012404
LOCUS       AC012404   199722 bp    DNA             HTG       26-MAY-2000
DEFINITION  Homo sapiens chromosome 15 clone RP11-39M21 map 15, WORKING DRAFT
            SEQUENCE, 6 unordered pieces.
ACCESSION   AC012404
VERSION     AC012404.4  GI:7107808
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 199722)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 15, clone RP11-39M21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 199722)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Feb 28, 2000 this sequence version replaced gi:6514012.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L2261
                Center clone name: 39_M_21
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 178894 bases at least Q40
                Consensus quality: 191626 bases at least Q30
                Consensus quality: 196426 bases at least Q20
                Insert size: 194000; agarose-fp
                Insert size: 199222; sum-of-contigs
                Quality coverage: 6.2 in Q20 bases; agarose-fp
                Quality coverage: 6.1 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     5729: contig of 5729 bp in length
            *    5730 5829: gap of      100 bp
            *    5830    20896: contig of 15067 bp in length
            *   20897 20996: gap of      100 bp
            *   20997    52603: contig of 31607 bp in length
            *   52604 52703: gap of      100 bp
            *   52704    89348: contig of 36645 bp in length
            *   89349 89448: gap of      100 bp
            *   89449   138760: contig of 49312 bp in length
            *  138761 138860: gap of      100 bp
            *  138861   199722: contig of 60862 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="15"
                     /map="15"
                     /clone="RP11-39M21"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .5729
                     /note="assembly_fragment"
     misc_feature    5830. .20896
                     /note="assembly_fragment"
     misc_feature    20997. .52603
                     /note="assembly_fragment"
     misc_feature    52704. .89348
                     /note="assembly_fragment
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                     vector_side:left"
     misc_feature    89449. .138760
                     /note="assembly_fragment"
     misc_feature    138861. .199722
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
BASE COUNT    60442 a  42775 c  40458 g  55547 t    500 others
ORIGIN


  Query Match             3.6%;  Score 189;  DB 71;  Length 199722;
  Best Local Similarity   80.1%;  Pred. No. 1.5e-30;
  Matches  222;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy   1290 tctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacctctgcctccc 1349
          |||||  |  | : |      || |    |   | || ||||| ||||||||||||||||||
Db 184619 TCTGTCGCCCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCCCTGCAACCTCTGCCTCCC 184678

Qy   1350 aggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacaggcgcacgccc 1409
          ||||||  |  |||||||| ||||||||||  |||||||||| |||| | |||| ||
Db 184679 AGGTTCGGGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAAGTGCACACCT 184738

Qy   1410 ggctaatttttgtattgttagtagagatggggtttcaccatattagcccggctggtcttg 1469
          |||||||||||||||  ||||||||||  |||||||||||||| ||| || ||||||||
Db 184739 GGCTAATTTTTGTATTTTTAGTAGAGAAAGGGTTTCACCATATTGGCCAGGGTGGTCTTG 184798

Qy   1470 aactcctgacctcaggtgatccacccacctcagcctcctaaagtgctgggattacaggca 1529
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db 184799 AACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCG 184858
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Qy   1530 tgagtcaccgcgcccggccaagggtcagtgtttaata 1566
          |||| ||||  ||| |||| |   | | | ||| | |
Db 184859 TGAGCCACCATGCCAGGCCCATTCTTACTTTTTTACA 184895
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RESULT 10
AC004973/c
LOCUS AC004973 97037 bp DNA PRI 21-DEC-1999
DEFINITION Homo sapiens PAC clone RP5-1139I1 from Xq23, complete sequence.
ACCESSION AC004973
VERSION AC004973.1 GI:3694660
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 97037)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE 2 (bases 1 to 97037)
AUTHORS Courtney,L., Langston,Y. and Drone,K.
TITLE The sequence of Homo sapiens PAC clone RP5-1139I1
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 97037)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 97037)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 97037)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 97037)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Oct 3, 1998 this sequence version replaced gi:3213024.
---------- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
---------- Summary Statistics
Center project name: H_DJ1139I01
----------.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the chromosome X mapping group at the Sanger Centre, Wellcome Trust Genome Campus, Hinxton, UK. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX/

SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP4-555N2; the clone sequenced to the right is RP3-404F18, 200 bp overlap. Actual start of this clone is at base position 1 of RP5-1139I1; actual end is at 13269 of RP3-404F18.

FEATURES Location/Qualifiers
source 1. .97037
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xq23"
/clone="RP5-1139I1"
/clone_lib="RPCI-5"
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/rpt_family="Alu"
repeat_region 2179. .2349
/rpt_family="MER1_type?"
repeat_region 3434. .3489
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repeat_region 3526. .3739
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repeat_region 4681. .4852
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repeat_region 5395. .5961
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repeat_region 6293. .6393
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repeat_region 6394. .7105
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repeat_region 7104. .7211
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repeat_region 7342. .7520
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repeat_region 7542. .7644
/rpt_family="Alu"
repeat_region 7645. .8674
/rpt_family="Retroviral"
repeat_region 8682. .9314
/rpt_family="Retroviral"
repeat_region 9315. .9368
/rpt_family="7SLRNA"
repeat_region 9371. .10157
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repeat_region 10165. .10817
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repeat_region 10818. .10973
/rpt_family="Alu"
repeat_region 10974. .11111
/rpt_family="L1"
repeat_region 11238. .11612
/rpt_family="MaLR"
repeat_region 11972. .12283
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repeat_region 12570. .12854
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repeat_region 12859. .13433
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  Query Match             3.5%;  Score 187.8;  DB 9;  Length 97037;
  Best Local Similarity   78.7%;  Pred. No. 2.6e-30;
  Matches  240;  Conservative    0;  Mismatches   57;  Indels    8;  Gaps    1;

Qy   1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
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Db  54922 AGAGTCTTGCTCTGTCATCCAAGCTGGAGTGCAGTGGCACGATCTCAGCTCACTGCAACC 54863

Qy   1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
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Db  54862 TCTGCCTCCTGGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGACTACAG 54803

Qy   1400 gcg--------cacgcccggctaatttttgtattgttagtagagatggggtttcaccata 1451
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Db  54802 GCGCATGCCACCACGCCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 54743

Qy   1452 ttagcccggctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaa 1511
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Db  54742 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGATGATCCACCTGCCTCGGCCTCCCAAA 54683

Qy   1512 gtgctgggattacaggcatgagtcaccgcgcccggccaagggtcagtgtttaataaggaa 1571
          ||||||||||||||||  |||| ||||||||||||||     |  || |||   || | |
Db  54682 GTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCTCTTCTAGGTATTTTGGAATGTA 54623

Qy   1572 taact 1576
            || |
Db  54622 CAATT 54618


RESULT  11
HUMYWXD703/c
LOCUS       HUMYWXD703 135038 bp    DNA             PRI       24-DEC-1996
DEFINITION  Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
ACCESSION   L78810
VERSION     L78810.1  GI:1381111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 135038)
  AUTHORS   Chen,C.N., Su,Y., Baybayan,P., Siruno,A., Nagaraja,R.,
            Mazzarella,R., Schlessinger,D. and Chen,E.
  TITLE     Ordered shotgun sequencing of a 135 kb Xq25 YAC containing ANT2 and
            four possible genes, including three confirmed by EST matches
  JOURNAL   Nucleic Acids Res. 24 (20), 4034-4041 (1996)
  MEDLINE   97078684
COMMENT     Submitted by:
            Ellson Chen,
            Advanced Center for Genetic Technology,
            Applied Biosystems Division of Perkin Elmer Corp., 850 Lincoln
            Center Drive,
            Foster City, CA 94404 USA
            and
            David Schlessinger,
            Department of Molecular Microbiology and Center for Genetics in
            Medicine
            Washington University School of Medicine,
            St. Louis MO 63110 USA
            e-mail: ellson@genseq.apldbio.com and davids@genetics.wustl.edu
            Note: Gene predictions were accomplished with runs of Grail
            versions 1.1 and 1.2, coupled with fasta and blastx comparisons to
            genbank & non-redundant peptide libraries. Repeat analysis was
            accomplished via censor.
            The Rat EST105369 shows significant homology via blastx to this
            sequence
            Strand Start  End
            top    9072   9326
            The Graves Disease carrier protein (X66035) shows significant
            homology via blastx to this sequence
            Strand Start End
            top 28802 29076
            top 35858 36081
            Comments for gene ANT-2 :
            This gene shows homology via blastx to the EST clone yl15a12 Strand
            Start End
            bottom 125256 125915.
FEATURES             Location/Qualifiers
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  Best Local Similarity   78.7%;  Pred. No. 2.6e-30;
  Matches  240;  Conservative    0;  Mismatches   57;  Indels    8;  Gaps    1;

Qy    1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
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Db    8349 AGAGTCTTGCTCTGTCATCCAAGCTGGAGTGCAGTGGCACGATCTCAGCTCACTGCAACC 8290

Qy    1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
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Db    8289 TCTGCCTCCTGGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGACTACAG 8230

Qy    1400 gcg--------cacgcccggctaatttttgtattgttagtagagatggggtttcaccata 1451
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Db    8229 GCGCATGCCACCACGCCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 8170

Qy    1452 ttagcccggctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaa 1511
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Db    8169 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGATGATCCACCTGCCTCGGCCTCCCAAA 8110

Qy    1512 gtgctgggattacaggcatgagtcaccgcgcccggccaagggtcagtgtttaataaggaa 1571
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Db    8109 GTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCTCTTCTAGGTATTTTGGAATGTA 8050

Qy    1572 taact 1576
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Db    8049 CAATT 8045


RESULT  12
HS821D11/c
LOCUS       HS821D11    76727 bp    DNA             PRI       12-DEC-1999
DEFINITION  Human DNA sequence from clone RP5-821D11 on chromosome 22q12.3-13.1
            Contains three partial unknown genes, one downstream of a predicted
            CpG island, and the first coding exon of the SREBF2 gene for Sterol
            Regulatory Element Binding Transcription Factor 2 downstream of a
            predicted CpG island, ESTs, STSs, GSSs and genomic marker D22S1157,
            complete sequence.
ACCESSION   AL021453
VERSION     AL021453.1  GI:3413288
KEYWORDS    HTG; D22S1157; SREBF2; Sterol Regulatory Element Binding
            Transcription Factor 2.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 76727)
  AUTHORS   Bird,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Aug 12, 1998 this sequence version replaced gi:3355590.
            This sequence has been finished according to sequence map criteria
            as follows. An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated human repeat sequence elements (e.g. Alu). Where the
            sequence is ambiguous, there is an annotation using the 'unsure'
            feature key.
            This sequence was generated from part of bacterial clone contigs of
            human chromosome 22, constructed by the Sanger Centre Chromosome 22
            Mapping Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr22
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP5-821D11 is
            from the library RPCI-5 constructed at the Roswell Park Cancer
            Institute by the group of Pieter de Jong. For further details see
            http://bacpac.med.buffalo.edu/
            VECTOR: pCYPAC2
            IMPORTANT: This sequence is not the entire insert of clone
            RP5-821D11 It may be shorter because we only sequence overlapping
            sections once, or longer because we arrange for a small overlap
            between neighbouring submissions.
            The true left end of clone RP5-821D11 is at 1 in this sequence. The
            true left end of clone CTA-250D10 is at 76628 in this sequence. The
            true right end of clone CTA-109G6 is at 42082 in this sequence. The
            start of this sequence overlaps with sequence Z99716 The end of
            this sequence overlaps with sequence Z83840.
FEATURES              Location/Qualifiers
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                      /clone_lib="RPCI-5"
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     repeat_region    435. .743
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     variation        446. .448
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                      this gene and dJ821D11.2 could be part of one gene
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     repeat_region   3458. .3551
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                /note="AluJb repeat: matches 1. .299 of consensus"
     repeat_region   3849. .3887
                /note="MIR repeat: matches 32. .74 of consensus"
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     repeat_region   4791. .5099
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                tt in this entry
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     variation       5107. .5112
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                /replace="tt"
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     variation       5359. .5361
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                /replace="ttat"
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                /replace="ttt"
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  Query Match              3.5%;  Score 185.8;  DB 65;  Length 76727;
  Best Local Similarity   78.5%;  Pred. No. 7e-30;
  Matches  238;  Conservative    0;  Mismatches   57;  Indels    8;  Gaps    1;

Qy   1280 agggtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacc 1339
          || ||     |||||  | ||  |     || |    |   | || |||| |||||||||
Db  57418 AGAGTCTCATTCTGTTGCCTAGGCTGGAGTGCAGTGGCATGATCTCAGCTTACTGCAACC 57359

Qy   1340 tctgcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacag 1399
          ||||||||||||||||||  |||||||||||||| ||||||  | || ||||||||||  ||
Db  57358 TCTGCCTCCCAGGTTCAAGTGATTCTCCTGTCTCTGCCTCCTGGGTTGCTGGGACTATAG 57299

Qy   1400 gcg--------cacgcccggctaatttttgtattgttagtagagatggggtttcaccata 1451
          |||        || |||||||||||||||||| ||||||||||||||||||||||||||
Db  57298 GCGTGTACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 57239

Qy   1452 ttagcccggctggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaa 1511
          || ||  |||||||||||||||||||||||||||||||| |||||||| |||||| |||
Db  57238 TTGGCTAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCGCCCACCTCGGCCTCCCAAA 57179

Qy   1512 gtgctgggattacaggcatgagtcaccgcgcccggccaagggtcagtgtttaataaggaa 1571
          |||||||||||||||||||| ||| | ||||||||||   || | || |   ||  ||
Db  57178 GTGCTGGGATTACAGGCATGAGCCACTGTGCCCGGCCAAAAATCTGGGTATTTCAAATAA 57119

Qy   1572 taa 1574
           ||
Db  57118 AAA 57116


RESULT  13
AC026395/c
LOCUS       AC026395   152044 bp    DNA             HTG       15-JUN-2000
DEFINITION  Homo sapiens chromosome 10 clone RP11-45D20, WORKING DRAFT
            SEQUENCE, 44 unordered pieces.
ACCESSION   AC026395
VERSION     AC026395.3  GI:8567738
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152044)
  AUTHORS   Smith,D.R.
  TITLE     Genome Therapeutics Corporation Sequencing Center: Human Genome
            Sequence Data
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 152044)
  AUTHORS   Smith,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
            Street, Waltham, MA 02453, USA
COMMENT     On Jun 15, 2000 this sequence version replaced gi:7330305.
            ---------- Genome Center
                       Center: Genome Therapeutics Corperation
                       Center code: GTC
                       Web site: http://www.genomecorp.com/
                       Contact: gtc-seqcenter@genomecorp.com
```

```
            -------------- Project Information
                Center project name: hg344
            -------------- Summary Statistics
                Sequencing vector: N/A
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 990315
                Consensus quality: 126801 bases at least Q40
                Consensus quality: 138138 bases at least Q30
                Consensus quality: 140422 bases at least Q20
                Insert size: 147744; sum-of-contigs
                Quality coverage: 3.2x in Q20 bases; sum-of-contigs
            --------------.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*        1     1006: contig of 1006 bp in length
*     1007     1106: gap of unknown length
*     1107     2475: contig of 1369 bp in length
*     2476     2575: gap of unknown length
*     2576     3927: contig of 1352 bp in length
*     3928     4027: gap of unknown length
*     4028     5333: contig of 1306 bp in length
*     5334     5433: gap of unknown length
*     5434     6564: contig of 1131 bp in length
*     6565     6664: gap of unknown length
*     6665     7870: contig of 1206 bp in length
*     7871     7970: gap of unknown length
*     7971     9384: contig of 1414 bp in length
*     9385     9484: gap of unknown length
*     9485    10791: contig of 1307 bp in length
*    10792    10891: gap of unknown length
*    10892    13010: contig of 2119 bp in length
*    13011    13110: gap of unknown length
*    13111    14617: contig of 1507 bp in length
*    14618    14717: gap of unknown length
*    14718    16217: contig of 1500 bp in length
*    16218    16317: gap of unknown length
*    16318    18106: contig of 1789 bp in length
*    18107    18206: gap of unknown length
*    18207    19498: contig of 1292 bp in length
*    19499    19598: gap of unknown length
*    19599    20867: contig of 1269 bp in length
*    20868    20967: gap of unknown length
*    20968    22203: contig of 1236 bp in length
*    22204    22303: gap of unknown length
*    22304    24098: contig of 1795 bp in length
*    24099    24198: gap of unknown length
*    24199    26005: contig of 1807 bp in length
*    26006    26105: gap of unknown length
*    26106    27441: contig of 1336 bp in length
*    27442    27541: gap of unknown length
*    27542    29037: contig of 1496 bp in length
*    29038    29137: gap of unknown length
*    29138    30660: contig of 1523 bp in length
*    30661    30760: gap of unknown length
*    30761    32755: contig of 1995 bp in length
*    32756    32855: gap of unknown length
*    32856    34483: contig of 1628 bp in length
*    34484    34583: gap of unknown length
*    34584    37578: contig of 2995 bp in length
*    37579    37678: gap of unknown length
*    37679    39699: contig of 2021 bp in length
*    39700    39799: gap of unknown length
*    39800    42411: contig of 2612 bp in length
*    42412    42511: gap of unknown length
*    42512    45638: contig of 3127 bp in length
*    45639    45738: gap of unknown length
*    45739    49739: contig of 4001 bp in length
*    49740    49839: gap of unknown length
*    49840    54276: contig of 4437 bp in length
*    54277    54376: gap of unknown length
*    54377    59051: contig of 4675 bp in length
*    59052    59151: gap of unknown length
*    59152    64626: contig of 5475 bp in length
*    64627    64726: gap of unknown length
*    64727    67988: contig of 3262 bp in length
*    67989    68088: gap of unknown length
*    68089    72494: contig of 4406 bp in length
*    72495    72594: gap of unknown length
*    72595    75643: contig of 3049 bp in length
*    75644    75743: gap of unknown length
*    75744    79510: contig of 3767 bp in length
*    79511    79610: gap of unknown length
*    79611    84664: contig of 5054 bp in length
*    84665    84764: gap of unknown length
*    84765    90514: contig of 5750 bp in length
*    90515    90614: gap of unknown length
*    90615    96185: contig of 5571 bp in length
*    96186    96285: gap of unknown length
*    96286   102048: contig of 5763 bp in length
*   102049   102148: gap of unknown length
*   102149   108361: contig of 6213 bp in length
*   108362   108461: gap of unknown length
*   108462   114329: contig of 5868 bp in length
*   114330   114429: gap of unknown length
*   114430   120644: contig of 6215 bp in length
*   120645   120744: gap of unknown length
*   120745   128025: contig of 7281 bp in length
*   128026   128125: gap of unknown length
*   128126   138788: contig of 10663 bp in length
*   138789   138888: gap of unknown length
*   138889   152044: contig of 13156 bp in length.
FEATURES             Location/Qualifiers
     source          1. .152044
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /clone="RP11-45D20"
                     /clone_lib="RPCI-11"
BASE COUNT    40176 a  33928 c  33229 g  40362 t   4349 others
ORIGIN


  Query Match             3.5%;  Score 185.8;  DB 79;  Length 152044;
  Best Local Similarity   80.8%;  Pred. No. 7.1e-30;
  Matches  232;  Conservative    0;  Mismatches   47;  Indels    8;  Gaps    1;

Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
           | ||  ||||||||||||||||  |||||| ||||||||  |||||||| ||||||||||
Db  30398 ATCTCGGCTCACTGCAACCTCCACCTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCC 30339

Qy   1381 cgcgtagctgggactacaggc--------gcacgcccggctaatttttgtattgttagta 1432
           | ||||||||| |||||||         ||||||| ||||||||||||||| ||||||
Db  30338 TGAGTAGCTGGGATTACAGGCACCCACTACCACGCCCAGCTAATTTTTGTATTTTTAGTA 30279

Qy   1433 gagatggggtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatcca 1492
           |||||||||||||||||| || ||| ||||||||||||||||||||||||||||||||
Db  30278 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 30219

Qy   1493 cccacctcagcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaagg 1552
           ||| ||| ||||||| |||||||||||||||||||||||| ||| || || ||||||
Db  30218 CCCGCCTTAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCACCTGGCCAATT 30159

Qy   1553 gtcagtgtttaataaggaataacttgaatggtttactaaaccaacag 1599
           | | | |||   | | || ||  || ||  ||||  |||   ||||
Db  30158 TTAATTTTTTTTAATGAAAAAATGTGGATATTTTAAAAAAAACACAG 30112


RESULT  14
AC025947/c
LOCUS       AC025947   157057 bp    DNA             HTG       10-JUN-2000
```

```
DEFINITION  Homo sapiens chromosome Chromosome 10 clone RP11-78A18, WORKING
            DRAFT SEQUENCE, 26 unordered pieces.
ACCESSION   AC025947
VERSION     AC025947.3  GI:8439851
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 157057)
  AUTHORS   Smith,D.R.
  TITLE     Genome Therapeutics Corporation Sequencing Center: Human Genome
            Sequence Data
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 157057)
  AUTHORS   Smith,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
            Street, Waltham, MA 02453, USA
COMMENT     On Jun 10, 2000 this sequence version replaced gi:7528340.
            -------------- Genome Center
                           Center: Genome Therapeutics Corperation
                           Center code: GTC
                           Web site: http://www.genomecorp.com/
                           Contact: gtc-seqcenter@genomecorp.com
                       -------------- Project Information
                           Center project name: hg307
                       -------------- Summary Statistics
                           Sequencing vector: N/A
                           Chemistry: Dye-terminator Big Dye; 100% of reads
                           Assembly program: Phrap; version 990315
                           Consensus quality: 140586 bases at least Q40
                           Consensus quality: 148596 bases at least Q30
                           Consensus quality: 150061 bases at least Q20
                           Insert size: 154557; sum-of-contigs
                           Quality coverage: 3.7x in Q20 bases; sum-of-contigs
                       --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 26 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1544: contig of 1544 bp in length
            *     1545     1644: gap of unknown length
            *     1645     3218: contig of 1574 bp in length
            *     3219     3318: gap of unknown length
            *     3319     5022: contig of 1704 bp in length
            *     5023     5122: gap of unknown length
            *     5123     6553: contig of 1431 bp in length
            *     6554     6653: gap of unknown length
            *     6654     8651: contig of 1998 bp in length
            *     8652     8751: gap of unknown length
            *     8752    10843: contig of 2092 bp in length
            *    10844    10943: gap of unknown length
            *    10944    13772: contig of 2829 bp in length
            *    13773    13872: gap of unknown length
            *    13873    15825: contig of 1953 bp in length
            *    15826    15925: gap of unknown length
            *    15926    19591: contig of 3666 bp in length
            *    19592    19691: gap of unknown length
            *    19692    22350: contig of 2659 bp in length
            *    22351    22450: gap of unknown length
            *    22451    25948: contig of 3498 bp in length
            *    25949    26048: gap of unknown length
            *    26049    29641: contig of 3593 bp in length
            *    29642    29741: gap of unknown length
            *    29742    34105: contig of 4364 bp in length
            *    34106    34205: gap of unknown length
            *    34206    38484: contig of 4279 bp in length
            *    38485    38584: gap of unknown length
            *    38585    41992: contig of 3408 bp in length
            *    41993    42092: gap of unknown length
            *    42093    47920: contig of 5828 bp in length
            *    47921    48020: gap of unknown length
            *    48021    54416: contig of 6396 bp in length
            *    54417    54516: gap of unknown length
            *    54517    60194: contig of 5678 bp in length
            *    60195    60294: gap of unknown length
            *    60295    67639: contig of 7345 bp in length
            *    67640    67739: gap of unknown length
            *    67740    74790: contig of 7051 bp in length
            *    74791    74890: gap of unknown length
            *    74891    85631: contig of 10741 bp in length
            *    85632    85731: gap of unknown length
            *    85732    93940: contig of 8209 bp in length
            *    93941    94040: gap of unknown length
            *    94041   104191: contig of 10151 bp in length
            *   104192   104291: gap of unknown length
            *   104292   116387: contig of 12096 bp in length
            *   116388   116487: gap of unknown length
            *   116488   135857: contig of 19370 bp in length
            *   135858   135957: gap of unknown length
            *   135958   157057: contig of 21100 bp in length.
FEATURES             Location/Qualifiers
     source          1. .157057
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="Chromosome 10"
                     /clone="RP11-78A18"
                     /clone_lib="RPCI-11"
BASE COUNT    45178 a  32550 c  32372 g  44448 t   2509 others
ORIGIN


  Query Match             3.5%;  Score 185.8;  DB 78;  Length 157057;
  Best Local Similarity   80.8%;  Pred. No. 7.1e-30;
  Matches  232;  Conservative    0;  Mismatches   47;  Indels    8;  Gaps    1;

Qy   1321 acctgagctcactgcaacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
          | ||  ||||||||||||||||  |||||| ||||||||  |||||||| ||||||||||
Db 109551 ATCTCGGCTCACTGCAACCTCCACCTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCC 109492

Qy   1381 cgcgtagctgggactacaggc--------gcacgcccggctaatttttgtattgttagta 1432
          | ||||||||| |||||||          ||||||| ||||||||||||||| |||||||
Db 109491 TGAGTAGCTGGGATTACAGGCACCCACTACCACGCCCAGCTAATTTTTGTATTTTTAGTA 109432

Qy   1433 gagatggggtttcaccatattagcccggctggtcttgaactcctgacctcaggtgatcca 1492
          |||||||||||||||||| || ||| ||||||||||||||||||||||||||||||||||
Db 109431 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 109372

Qy   1493 cccacctcagcctcctaaagtgctgggattacaggcatgagtcaccgcgcccggccaagg 1552
          ||| ||| ||||||| |||||||||||||||||||||||| ||| || || ||||||
Db 109371 CCCGCCTTAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCACCTGGCCAATT 109312

Qy   1553 gtcagtgtttaataaggaataacttgaatggtttactaaaccaacag 1599
          | | | |||   | | || ||  || ||  |||| |||  ||||
Db 109311 TTAATTTTTTTTAATGAAAAAATGTGGATATTTTAAAAAAAACACAG 109265


RESULT  15
AC015488
LOCUS       AC015488   161499 bp    DNA             HTG       16-MAR-2000
DEFINITION  Homo sapiens clone RP11-20F6, WORKING DRAFT SEQUENCE, 16 unordered
            pieces.
ACCESSION   AC015488
VERSION     AC015488.4  GI:7107977
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 161499)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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  TITLE     Homo sapiens, clone RP11-20F6
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 161499)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Feb 28, 2000 this sequence version replaced gi:6715933.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L3895
                Center clone name: 20_F_6
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 152793 bases at least Q40
                Consensus quality: 156653 bases at least Q30
                Consensus quality: 158136 bases at least Q20
                Insert size: 160000; agarose-fp
                Insert size: 159999; sum-of-contigs
                Quality coverage: 5.9 in Q20 bases; agarose-fp
                Quality coverage: 5.9 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 16 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2206: contig of 2206 bp in length
            *     2207 2306: gap of      100 bp
            *     2307     6910: contig of 4604 bp in length
            *     6911 7010: gap of      100 bp
            *     7011     9818: contig of 2808 bp in length
            *     9819 9918: gap of      100 bp
            *     9919    13394: contig of 3476 bp in length
            *    13395 13494: gap of      100 bp
            *    13495    17122: contig of 3628 bp in length
            *    17123 17222: gap of      100 bp
            *    17223    19752: contig of 2530 bp in length
            *    19753 19852: gap of      100 bp
            *    19853    23958: contig of 4106 bp in length
            *    23959 24058: gap of      100 bp
            *    24059    29684: contig of 5626 bp in length
            *    29685 29784: gap of      100 bp
            *    29785    33951: contig of 4167 bp in length
            *    33952 34051: gap of      100 bp
            *    34052    39841: contig of 5790 bp in length
            *    39842 39941: gap of      100 bp
            *    39942    48297: contig of 8356 bp in length
            *    48298 48397: gap of      100 bp
            *    48398    56898: contig of 8501 bp in length
            *    56899 56998: gap of      100 bp
            *    56999    65924: contig of 8926 bp in length
            *    65925 66024: gap of      100 bp
            *    66025    81114: contig of 15090 bp in length
            *    81115 81214: gap of      100 bp
            *    81215   112500: contig of 31286 bp in length
            *   112501 112600: gap of      100 bp
            *   112601   161499: contig of 48899 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP11-20F6"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .2206
                     /note="assembly_fragment"
     misc_feature    2307. .6910
                     /note="assembly_fragment"
     misc_feature    7011. .9818
                     /note="assembly_fragment"
     misc_feature    9919. .13394
                     /note="assembly_fragment"
     misc_feature    13495. .17122
                     /note="assembly_fragment"
     misc_feature    17223. .19752
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     misc_feature    19853. .23958
                     /note="assembly_fragment"
     misc_feature    24059. .29684
                     /note="assembly_fragment"
     misc_feature    29785. .33951
                     /note="assembly_fragment"
     misc_feature    34052. .39841
                     /note="assembly_fragment"
     misc_feature    39942. .48297
                     /note="assembly_fragment"
     misc_feature    48398. .56898
                     /note="assembly_fragment"
     misc_feature    56999. .65924
                     /note="assembly_fragment"
     misc_feature    66025. .81114
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    81215. .112500
                     /note="assembly_fragment"
     misc_feature    112601. .161499
                     /note="assembly_fragment"
BASE COUNT    44611 a  37543 c  36473 g  41370 t   1502 others
ORIGIN


  Query Match             3.5%;  Score 185.8;  DB 72;  Length 161499;
  Best Local Similarity   77.1%;  Pred. No. 7.1e-30;
  Matches  226;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy   1283 gtgagggtctgtgtcttacacctacctgtatgctctacacctgagctcactgcaacctct 1342
          ||   | |||||  |  |  |       | |    |  || ||  ||||||||||||||||
Db  16769 GTCTTGCTCTGTCACCCAGGCTGGAGGGCAGTGGCACCATCTCGGCTCACTGCAACCTCT 16828

Qy   1343 gcctcccaggttcaagcaattctcctgtctcagcctcccgcgtagctgggactacaggcg 1402
          |||||||||| |||||||||||||||||| |||||||||| | ||| |||||  || ||||
Db  16829 GCCTCCCAGATTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTACCTGGGGTTATAGGCA 16888

Qy   1403 cacgcccggctaatttttgtattgttagtagagatggggtttcaccatattagcccggct 1462
          || ||| |||||||||||| || ||||||||||||||||||  |||| || ||| ||||
Db  16889 CATGCCAGGCTAATTTTTGTGTTTTTAGTAGAGATGGGGTTTTGCCATGTTGGCCAGGCT 16948

Qy   1463 ggtcttgaactcctgacctcaggtgatccacccacctcagcctcctaaagtgctgggatt 1522
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          ||||||||||||||||||||||| |||||| ||| |||| |||||| ||||||||||||||
Db  16949 GGTCTTGAACTCCTGACCTCAGATGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATT 17008

Qy   1523 acaggcatgagtcaccgcgcccggccaagggtcagtgtttaataaggaataac 1575
          |||||  |||| |||||||||| ||| |    | | | |||| |    |  |||
Db  17009 ACAGGTGTGAGCCACCGCGCCCAGCCTATTTTTAATTTTTATTTTTTATCAAC 17061
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Job time: 40455 sec